

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	311	100.0	311	4	US-09-634-955B-5	Sequence 5, Appli
2	311	100.0	311	4	US-09-816-760-5	Sequence 5, Appli
3	311	100.0	311	4	US-09-838-561-5	Sequence 5, Appli
4	52	16.7	311	4	US-09-838-561-15	Sequence 15, Appl
5	9	2.9	682	4	US-09-107-532A-4499	Sequence 4499, Ap
6	9	2.9	1170	4	US-09-462-136-6	Sequence 6, Appli
7	8	2.6	113	3	US-08-905-223-439	Sequence 439, App
8	8	2.6	261	4	US-09-328-352-7731	Sequence 7731, Ap
9	8	2.6	263	4	US-09-270-767-46093	Sequence 46093, A
10	8	2.6	299	4	US-09-902-540-14916	Sequence 14916, A
11	8	2.6	310	4	US-09-907-794A-153	Sequence 153, App
12	8	2.6	310	4	US-09-905-125A-153	Sequence 153, App
13	8	2.6	310	4	US-09-902-775A-153	Sequence 153, App
14	8	2.6	310	4	US-09-906-700-153	Sequence 153, App
15	8	2.6	310	4	US-09-903-603A-153	Sequence 153, App
16	8	2.6	310	4	US-09-904-920A-153	Sequence 153, App
17	8	2.6	310	4	US-09-909-064-153	Sequence 153, App

Database : Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

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SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1607	100.0		311	4	US-09-634-955B-5	Sequence 5, Appli
2	1607	100.0		311	4	US-09-816-760-5	Sequence 5, Appli
3	1607	100.0		311	4	US-09-838-561-5	Sequence 5, Appli
4	1467	91.3		311	4	US-09-838-561-15	Sequence 15, Appl
5	651.5	40.5		310	4	US-09-907-794A-153	Sequence 153, App
6	651.5	40.5		310	4	US-09-905-125A-153	Sequence 153, App
7	651.5	40.5		310	4	US-09-902-775A-153	Sequence 153, App
8	651.5	40.5		310	4	US-09-906-700-153	Sequence 153, App
9	651.5	40.5		310	4	US-09-903-603A-153	Sequence 153, App
10	651.5	40.5		310	4	US-09-904-920A-153	Sequence 153, App
11	651.5	40.5		310	4	US-09-909-064-153	Sequence 153, App
12	651.5	40.5		310	4	US-09-905-381A-153	Sequence 153, App
13	651.5	40.5		310	4	US-09-906-618-153	Sequence 153, App

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	52	16.7	223	2	Q8CHS7	Q8chs7 mus musculu	
2	9	2.9	281	1	CG11_RAT	P97586 rattus norv	
3	9	2.9	1170	2	Q12200	Q12200 saccharomyc	
4	8	2.6	83	1	YORC_TTV1	P19287 thermoprote	
5	8	2.6	134	2	Q89T92	Q89t92 bradyrhizob	
6	8	2.6	137	2	Q6ZTJ1	Q6ztj1 homo sapien	
7	8	2.6	150	2	Q747K4	Q747k4 geobacter s	
8	8	2.6	216	2	Q72RN4	Q72rn4 leptospira	
9	8	2.6	216	2	Q8F428	Q8f428 leptospira	
10	8	2.6	226	2	Q8MT30	Q8mt30 drosophila	
11	8	2.6	233	2	Q9CHT7	Q9cht7 lactococcus	
12	8	2.6	235	2	Q6XHS1	Q6xhs1 drosophila	
13	8	2.6	237	2	Q6IDG8	Q6idg8 drosophila	
14	8	2.6	244	2	Q8D3B0	Q8d3b0 wiggleswort	

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	9	2.9	1170	2	S52525	probable membrane
2	8	2.6	233	2	G86703	oxidoreductase ygc
3	8	2.6	260	2	E70881	probable fabG5 pro
4	8	2.6	261	2	G82082	conserved hypothet
5	8	2.6	262	2	T34378	hypothetical prote
6	8	2.6	293	2	T19954	hypothetical prote
7	8	2.6	325	2	T17307	hypothetical prote
8	8	2.6	341	2	D70761	probable fatty-acy
9	8	2.6	371	2	A44122	alpha-helical coil
10	8	2.6	938	2	T34105	hypothetical prote
11	8	2.6	964	2	AG3433	diguanylate cyclas
12	7	2.3	135	2	G89751	protein C33E10.10
13	7	2.3	141	2	C97338	hydroxymyristoyl-(
14	7	2.3	146	2	G97030	probable membrane
15	7	2.3	148	2	F86899	hypothetical prote
16	7	2.3	151	2	D75347	hypothetical prote
17	7	2.3	157	2	C71477	probable ribityllu
18	7	2.3	167	2	D82561	probable signal pe
19	7	2.3	184	2	B72601	hypothetical prote
20	7	2.3	198	2	B82080	flavodoxin [simila
21	7	2.3	200	2	T42066	glutamate-ammonia

Database : PIR_79:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	640.5	39.9		325	2	T17307	hypothetical prote
2	311.5	19.4		537	2	T34380	hypothetical prote
3	307	19.1		262	2	T34378	hypothetical prote
4	299.5	18.6		278	2	E83152	probable short-cha
5	274	17.1		277	2	AG1983	hypothetical prote
6	265.5	16.5		263	2	AI1692	oxidoreductase hom
7	265.5	16.5		266	2	H97309	short-chain alcoho
8	255.5	15.9		263	2	AH1321	oxidoreductase hom
9	253	15.7		259	2	A69965	ketoacyl reductase
10	249	15.5		259	2	B83838	oxidoreductase BH1
11	245	15.2		293	2	AD2176	oxidoreductase all
12	242	15.1		270	2	E86788	oxidoreductase yne
13	241.5	15.0		328	2	F75374	probable ketoacyl
14	241	15.0		247	2	F90254	hypothetical prote
15	241	15.0		253	2	A95223	hypothetical prote
16	238.5	14.8		287	2	C55210	hetN protein - Ana
17	235.5	14.7		287	2	AF2475	ketoacyl reductase
18	234.5	14.6		307	2	E70082	glucose 1-dehydrog
19	234	14.6		261	1	A28788	actinorhodin polyk
20	233	14.5		332	2	S37652	follicular lymphom

OM protein - protein search, using sw model

Run on: March 12, 2005, 13:06:08 ; Search time 174 Seconds
(without alignments)
915.268 Million cell updates/sec

Title: US-10-664-506-5
Perfect score: 1607
Sequence: 1 MGVMAMLMPLLLLLGISGLL.....FFFAVVACGVKEKLNVP EEG 311

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1017	63.3	223	2	Q8CHS7	Q8chs7 mus musculu	
2	651.5	40.5	310	2	Q6UX59	Q6ux59 homo sapien	
3	651.5	40.5	325	2	Q9BTF9	Q9btf9 homo sapien	
4	650.5	40.5	325	2	Q6IAN0	Q6ian0 homo sapien	
5	640.5	39.9	325	2	Q9UFM6	Q9ufm6 homo sapien	
6	625.5	38.9	323	2	Q99J47	Q99j47 m similar t	
7	557	34.7	291	2	Q9Y3A1	Q9y3a1 homo sapien	
8	466	29.0	326	2	Q9Y140	Q9y140 drosophila	
9	458	28.5	317	2	Q7Q732	Q7q732 anopheles g	
10	331	20.6	311	2	Q65ZI3	Q65zi3 caenorhabdi	
11	322	20.0	264	2	Q81M93	Q81m93 bacillus an	
12	321	20.0	264	2	Q635E8	Q635e8 bacillus ce	
13	320	19.9	264	2	Q731G1	Q731g1 bacillus ce	
14	311.5	19.4	537	2	Q22787	Q22787 caenorhabdi	
15	309	19.2	264	2	Q6HE26	Q6he26 bacillus th	

16	302.5	18.8	268	2	Q6F8F2	Q6f8f2	acinetobact
17	299.5	18.6	278	2	Q9HX59	Q9hx59	pseudomonas
18	295.5	18.4	339	1	DHS7_HUMAN	Q9y394	homo sapien
19	295.5	18.4	375	2	Q659E8	Q659e8	homo sapien
20	290.5	18.1	267	2	Q8EJM5	Q8ejm5	shewanella
21	288.5	18.0	324	2	Q6I7R1	Q6i7r1	rattus norv
22	286.5	17.8	260	2	O15744	O15744	dictyosteli
23	282	17.5	338	1	DHS7_MOUSE	Q9cxr1	mus musculu
24	277	17.2	273	2	Q6W1F0	Q6w1f0	rhizobium s
25	276	17.2	336	2	Q6GP08	Q6gp08	xenopus lae
26	274	17.1	277	2	Q8YX01	Q8yx01	anabaena sp
27	271	16.9	268	2	Q6CNU5	Q6cnu5	kluveromyc
28	265.5	16.5	263	2	Q92A39	Q92a39	listeria in
29	265.5	16.5	266	2	Q97DY5	Q97dy5	clostridium
30	263	16.4	298	2	Q87XV8	Q87xv8	pseudomonas
31	262.5	16.3	260	2	Q65HP3	Q65hp3	bacillus li
32	260.5	16.2	263	2	Q71Y45	Q71y45	listeria mo
33	258	16.1	312	2	Q9N126	Q9n126	bos taurus
34	258	16.1	316	2	Q8T197	Q8t197	dictyosteli
35	256	15.9	280	2	Q65F58	Q65f58	bacillus li
36	255.5	15.9	248	2	Q9RH22	Q9rh22	zymomonas m
37	255.5	15.9	263	2	Q8Y5S9	Q8y5s9	listeria mo
38	254	15.8	303	2	Q6F7B8	Q6f7b8	acinetobact
39	253	15.7	259	1	YQJQ_BACSU	P54554	bacillus su
40	253	15.7	295	2	Q8RR58	Q8rr58	acinetobact
41	252	15.7	295	2	P94129	P94129	acinetobact
42	250.5	15.6	271	2	Q7UPD8	Q7upd8	rhodopirell
43	249.5	15.5	311	2	Q9NYR8	Q9nyr8	homo sapien
44	249	15.5	259	2	Q9KCR3	Q9kcr3	bacillus ha
45	247	15.4	276	2	Q9ALU7	Q9alu7	enterobacte

ALIGNMENTS

RESULT 1

Q8CHS7

ID Q8CHS7 PRELIMINARY; PRT; 223 AA.

AC Q8CHS7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Similar to CGI-86 protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Mammary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,


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      ||| |||: ||||| |||||:|::: ||:| | : ||:
Db      181 QGKMSIPFRSAYAASKHATQAFDCLRAEMEQEYIEVTVISPGYIHTNLSVNAITADGS- 239

Qy      237 EASIWKFFFRKLTYG-----HPVEVAEEVMRTVRRKKQEVFMANPIPKAAVYVRT 287
      ||| |||||:|:| | :||::| :|: | ||:|
Db      240 -----RYGVMDDTTTAQGRSPVEVAQDVLAAVGKKKKDVIILADLLPSLAVYLRT 287

Qy      288 FFPEFFFAVVACGVKEK 304
      | ||::| :::
Db      288 LAPGLEFFSLMASRARKE 304

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09BTF9

AC 09BTF9:

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE DKFZP5660084 protein.

GN Name=DKFZp5660084;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson B.D., Mullahy S.J.

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.

RA Richards S. Worley K. C. Hale S. Garcia A. M. Gay L. J. Hulyk S. W.

RA Villalon D.K. Muzny D.M. Sodergren E.J. Lu X. Gibbs B.A.

RA Fahey J Helton E Kettelman M Madan A Rodrigues S Sanchez A

BA Whiting M. Madan A. Young A. C. Shevchenko Y. Bouffard G. G.

RA Blakesley B W Touchman J W Green F D Dickson M C

BA Rodriguez A C Grimwood J Schmutz J Myers B M Butterfield V S

BA Krzywinski M J Skalska H Smailus D E Schnorrich A Schein J E

BA Jones S I Marra M A

BT "Generation and initial analysis of more than 15,000 full length human

RT Generation and initial analysis of
BT and mouse cDNA sequences."

BI Proc Natl Acad Sci U S A 99:16000-16003 (2002)

RL	PFO
RN	[31]

RN	[2]
RR	SEQUENCE FROM N. A.

RP SEQUENCE FROM
PC TISSUE LINES

RC TISSUE=Lung;
RA Streusberg, B

RA Strausberg R.;
FI Submitted (MAR 2001) to the FBI/C. D. I./DOPI 101

RL	Sub
RN	[21]

RN	[3]
ED	SEQUENCE FROM N-1

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	311	100.0	311	4	AAB47593	Aab47593 Human DHD
2	311	100.0	311	6	ABP58046	Abp58046 Human deh
3	311	100.0	311	8	ADG40199	Adg40199 Human deh
4	255	82.0	311	3	AAB08911	Aab08911 Human sec
5	255	82.0	345	3	AAB08948	Aab08948 Human sec
6	156	50.2	246	8	ADM33425	Adm33425 Human PRO
7	107	34.4	118	4	AAM24151	Aam24151 Human EST
8	70	22.5	81	8	ABO54789	Abo54789 Human gen
9	52	16.7	311	6	ABP58047	Abp58047 Mouse deh
10	52	16.7	311	8	ADG40201	Adg40201 Mouse deh
11	29	9.3	29	3	AAB08949	Aab08949 Human sec
12	9	2.9	31	6	ADA98202	Ada98202 Human sec
13	9	2.9	31	6	ADA44050	Ada44050 Human sec
14	9	2.9	31	7	ADC20368	Adc20368 Human sec
15	9	2.9	31	7	ADF10701	Adf10701 Human sec
16	9	2.9	32	4	AAB60717	Aab60717 Human sec
17	9	2.9	281	2	AAW38423	Aaw38423 Rat cell
18	9	2.9	281	7	ADE62861	Ade62861 Rat Prote

RESULT 4

AAB08911

ID AAB08911 standard; protein; 311 AA.

XX

AC AAB08911;

XX

DT 30-AUG-2000 (first entry)

XX

DE Human secreted protein sequence encoded by gene 21 SEQ ID NO:68.

XX

KW Human; secreted protein; cytostatic; anti-proliferative; vulnerary;
KW immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;
KW hyperproliferative disorder; infectious disease; tissue regeneration;
KW screening; food additive; preservative; wound healing;
KW hyper-vascular disease; chromosome 11.

XX

OS Homo sapiens.

XX

PN WO200017222-A1.

XX

PD 30-MAR-2000.

XX

PF 22-SEP-1999; 99WO-US022012.

XX

PR 23-SEP-1998; 98US-0101546P.

PR 02-OCT-1998; 98US-0102895P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ruben SM, Rosen CA, Duan RD, Shi Y, Lafleur DW, Young PE, Ni J;
PI Komatsoulis G, Endress GA, Soppet DR;

XX

DR WPI; 2000-283538/24.

DR N-PSDB; AAA39072.

XX

PT Human secreted proteins and coding sequences useful in diagnostic and
PT therapeutic methods for disorders such as immune system or proliferative
PT disorders, related to the proteins.

XX

PS Claim 11; Page 366-367; 416pp; English.

XX

CC The polynucleotide sequences given in AAA39052 to AAA39088 encode the
CC human secreted proteins given in AAB08891 to AAB08984. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic; anti-
CC proliferative; immunosuppressive; antibacterial; and vulnerary. The
CC secreted proteins and their related polynucleotide sequences are useful
CC for diagnostic and therapeutic methods useful for diagnosing and treating
CC disorders related to the secreted proteins. The proteins, and
CC polynucleotide sequences may be useful for treating disorders of the
CC immune system, hyperproliferative disorders, infectious disease,
CC regeneration of tissues, for chemotaxis and for screening molecules that
CC bind to the proteins. The proteins or polynucleotide sequences may be
CC used as food additives or preservatives, to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, co-factors or other nutritional components. Agonists or
CC antagonists of the proteins may be used to prevent scar tissue growth

CC during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051
CC and AAB08890 are sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 311 AA;

Query Match 82.0%; Score 255; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 2e-231;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGVMAMLMPLLLLLGISGLLFIYQEVSRWSKSAVQNKVVVITDAISGLGKECARVFHTG	60
Db	1	MGVMAMLMPLLLLLGISGLLFIYQEVSRWSKSAVQNKVVVITDAISGLGKECARVFHTG	60
Qy	61	GARLVLCGKNWERLENLYDALISVADPSKTFTPKLVLLDLSDISCVPDVAKEVLDCYGC	120
Db	61	GARLVLCGKNWERLENLYDALISVADPSKTFTPKLVLLDLSDISCVPDVAKEVLDCYGC	120
Qy	121	DILINNASVKVKGPAHKISLELDKKIMDANYFGPITLTKALLPNMISRRTGQIVLVNNIQ	180
Db	121	DILINNASVKVKGPAHKISLELDKKIMDANYFGPITLTKALLPNMISRRTGQIVLVNNIQ	180
Qy	181	GKFGIPFRTTYAASKHAALGFFDCLRAEVEEYDVVISTVSPTFIRSYHVYPEQGNWEASI	240
Db	181	GKFGIPFRTTYAASKHAALGFFDCLRAEVEEYDVVISTVSPTFIRSYHVYPEQGNWEASI	240
Qy	241	WKFFFRKLTYGVHPV	255
Db	241	WKFFFRKLTYGVHPV	255

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	311	100.0	311	9	US-09-838-561-5	Sequence 5, Appli	
2	311	100.0	311	9	US-09-816-760-5	Sequence 5, Appli	
3	311	100.0	311	14	US-10-172-585-5	Sequence 5, Appli	
4	311	100.0	311	15	US-10-144-433-2	Sequence 2, Appli	
5	311	100.0	311	15	US-10-664-506-5	Sequence 5, Appli	
6	311	100.0	311	15	US-10-144-433-2	Sequence 2, Appli	
7	255	82.0	311	9	US-09-820-893-68	Sequence 68, Appl	
8	255	82.0	311	15	US-10-607-565-68	Sequence 68, Appl	
9	255	82.0	345	9	US-09-820-893-106	Sequence 106, App	
10	255	82.0	345	15	US-10-607-565-106	Sequence 106, App	

RESULT 1
 AI091419/c
 LOCUS AI091419 631 bp mRNA linear EST 30-OCT-1998
 DEFINITION ow62e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE:1651420 3' similar to WP:T25G12.7 CE07544 DEHYDROGENASE
 ;contains TAR1.t3 MER22 repetitive element ;; mRNA sequence.
 ACCESSION AI091419
 VERSION AI091419.1 GI:3430478
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 631)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1044 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 453.

FEATURES Location/Qualifiers
 source 1..631
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1651420"
 /lab_host="DH10B"
 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and cloneIDs: Soares NbHSF pool 1:
 309384-310919, 323208-325895 Soares Nb2HP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152327 Soares Nb2HF8-9W pool 1:
 758280-760583, 772104-774407 Soares NbHPA pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NbHOT
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 45.0%; Score 621; DB 1; Length 631;
 Best Local Similarity 100.0%; Pred. No. 5.9e-294;
 Matches 621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 698 TCATCAACAATGCCAGTGTGAAGGTGAAGGGGCTGCCATAAGATTTCTCTGGAGCTCG 757
 |||

Db	621	TCATCAACAATGCCAGTGTGAAGGTGAAGGGGCTGCCCATAGATTTCTCTGGAGCTCG	562
Qy	758	ACAAAAAGATCATGGATGCCAATTACTTTGGCCCCATCACATTGACGAAAGCCCTGCTTC	817
Db	561	ACAAAAAGATCATGGATGCCAATTACTTTGGCCCCATCACATTGACGAAAGCCCTGCTTC	502
Qy	818	CCAACATGATCTCCCGGAGAACAGGCCAAATCGTGTTAGTGAATAATATCCAAGGGAAGT	877
Db	501	CCAACATGATCTCCCGGAGAACAGGCCAAATCGTGTTAGTGAATAATATCCAAGGGAAGT	442
Qy	878	TTGGAATCCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGGCTTCTTTG	937
Db	441	TTGGAATCCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGGCTTCTTTG	382
Qy	938	ACTGCCTCCGAGCCGAAGTGGAGGAATACGATGTTGTTCATCAGCACCGTGAGCCCGACTT	997
Db	381	ACTGCCTCCGAGCCGAAGTGGAGGAATACGATGTTGTTCATCAGCACCGTGAGCCCGACTT	322
Qy	998	TCATCCGGTCGTACCACGTGTATCCAGAGCAAGGAACTGGGAAGCTTCCATTTGGAAAT	1057
Db	321	TCATCCGGTCGTACCACGTGTATCCAGAGCAAGGAACTGGGAAGCTTCCATTTGGAAAT	262
Qy	1058	TCTTTTTTCAGGAAGCTGACCTACGGCGTGACCCAGTAGAGGTGGCGGAGGAGGTGATGC	1117
Db	261	TCTTTTTTCAGGAAGCTGACCTACGGCGTGACCCAGTAGAGGTGGCGGAGGAGGTGATGC	202
Qy	1118	GCACCGTGCGGAGGAAGAAGCAAGAGGTGTTTATGGCCAACCCCATCCCCAAGGCCGCCG	1177
Db	201	GCACCGTGCGGAGGAAGAAGCAAGAGGTGTTTATGGCCAACCCCATCCCCAAGGCCGCCG	142
Qy	1178	TGTACGTCCGCACCTTCTTCCCGAGTTCTTTTTCGCCGTGGTGGCCTGTGGGGTGAAGG	1237
Db	141	TGTACGTCCGCACCTTCTTCCCGAGTTCTTTTTCGCCGTGGTGGCCTGTGGGGTGAAGG	82
Qy	1238	AGAAGCTCAATGTCCCGGAGGAGGGGTAACTGCAGGAGGCCAAATGGGGCCACCCCTTGGA	1297
Db	81	AGAAGCTCAATGTCCCGGAGGAGGGGTAACTGCAGGAGGCCAAATGGGGCCACCCCTTGGA	22
Qy	1298	AATAAAGGTTTTTCTGGCAA 1318	
Db	21	AATAAAGGTTTTTCTGGCAA 1	

RESULT 2
 AI741629/c
 LOCUS AI741629 632 bp mRNA linear EST 19-DEC-1999
 DEFINITION wg28f07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE:2366437 3' similar to WP:T25G12.7 CE07544 DEHYDROGENASE
 ;contains TAR1.t3 MER22 repetitive element ;; mRNA sequence.
 ACCESSION AI741629
 VERSION AI741629.1 GI:5109917
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 632)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1035 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 444.

FEATURES Location/Qualifiers
 source 1..632
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2366437"
 /lab_host="DH10B"
 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and cloneIDs: Soares NbHSF pool 1:
 309384-310919, 323208-325895 Soares Nb2HP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-152327 Soares Nb2HF8-9W pool 1:
 758280-760583, 772104-774407 Soares NbHPA pool 1:
 304776-306311, 320136-322823, 326280-326663 Soares NbHOT
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 40.0%; Score 551; DB 1; Length 632;
 Best Local Similarity 99.8%; Pred. No. 1.7e-259;
 Matches 601; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 705 CAATGCCAGTGTGAAGGTGAAGGGCCTGCCCATAGATTCTCTGGAGCTCGACAAAAA 764
 |||

Db	615	CAATGCCAGTGTGAAGGTGAAGGGGCTGCCATAAGATTTCTCTGGAGCTCGACAGAAA	556
Qy	765	GATCATGGATGCCAATTACTTTGGCCCCATCACATTGACGAAAGCCCTGCTTCCCAACAT	824
Db	555	GATCATGGATGCCAATTACTTTGGCCCCATCACATTGACGAAAGCCCTGCTTCCCAACAT	496
Qy	825	GATCTCCCGGAGAAACAGGCCAAATCGTGTTAGTGAATAATATCCAAGGGAAGTTTGGAAT	884
Db	495	GATCTCCCGGAGAAACAGGCCAAATCGTGTTAGTGAATAATATCCAAGGGAAGTTTGGAAT	436
Qy	885	CCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGGCTTCTTTGACTGCCT	944
Db	435	CCCGTTCCGTACGACTTACGCTGCCTCCAAGCACGCAGCCCTGGGCTTCTTTGACTGCCT	376
Qy	945	CCGAGCCGAAGTGGAGGAATACGATGTTGTCATCAGCACCGTGAGCCCGACTTTTCATCCG	1004
Db	375	CCGAGCCGAAGTGGAGGAATACGATGTTGTCATCAGCACCGTGAGCCCGACTTTTCATCCG	316
Qy	1005	GTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTTGGAAATTCTTTTTT	1064
Db	315	GTCGTACCACGTGTATCCAGAGCAAGGAAACTGGGAAGCTTCCATTTGGAAATTCTTTTTT	256
Qy	1065	CAGGAAGCTGACCTACGGCGTGACCCAGTAGAGGTGGCGGAGGAGGTGATGCGCACCGT	1124
Db	255	CAGGAAGCTGACCTACGGCGTGACCCAGTAGAGGTGGCGGAGGAGGTGATGCGCACCGT	196
Qy	1125	GCGGAGGAAGAAGCAAGAGGTGTTTATGGCCAACCCCATCCCCAAGGCCGCCGTGTACGT	1184
Db	195	GCGGAGGAAGAAGCAAGAGGTGTTTATGGCCAACCCCATCCCCAAGGCCGCCGTGTACGT	136
Qy	1185	CCGCACCTTCTTCCCGGAGTTCTTTTTTCGCCGTGGTGGCCTGTGGGGTGAAGGAGAAGCT	1244
Db	135	CCGCACCTTCTTCCCGGAGTTCTTTTTTCGCCGTGGTGGCCTGTGGGGTGAAGGAGAAGCT	76
Qy	1245	CAATGTCCCGGAGGAGGGGTAACTGCAGGAGGCCAAATGGGCCACCCCTTGGAAATAAAG	1304
Db	75	CAATGTCCCGGAGGAGGGGTAACTGCAGGAGGCCAAATGGGCCACCCCTTGGAAATAAAG	16
Qy	1305	GT	1306
Db	15	GT	14

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	1379	100.0	1379	4	AAH43561	Aah43561 Human DHD	
2	1379	100.0	1379	10	ABV76050	Abv76050 Human deh	
3	1379	100.0	1379	12	ADG40198	Adg40198 cDNA enco	
4	1004	72.8	1114	8	ABX71069	Abx71069 Novel hum	
5	955	69.3	1157	3	AAA39072	Aaa39072 Human sec	
6	936	67.9	936	4	AAH43565	Aah43565 Human DHD	
7	677	49.1	797	12	ADM33424	Adm33424 Human PRO	
8	327	23.7	780	4	AAH98810	Aah98810 Human EST	
9	208	15.1	247	12	ACH82344	Ach82344 Human gen	
10	208	15.1	514	12	ACH68644	Ach68644 Human gen	
c 11	159	11.5	599	12	ACH69248	Ach69248 Human gen	

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID		Description	
1	1379	100.0	1379	6	AR278046		AR278046 Sequence	
2	1379	100.0	1379	6	AR392052		AR392052 Sequence	
3	1379	100.0	1379	6	AR403912		AR403912 Sequence	
4	1379	100.0	1379	6	AX320639		AX320639 Sequence	
5	1004	72.8	1114	6	AR542048		AR542048 Sequence	
6	955	69.3	1157	6	BD233739		BD233739 31 human	
7	933	67.7	933	6	AR278047		AR278047 Sequence	
8	933	67.7	933	6	AR392053		AR392053 Sequence	
9	933	67.7	933	6	AR403913		AR403913 Sequence	
10	933	67.7	933	6	AX320641		AX320641 Sequence	
11	932	67.6	932	6	CQ731016		CQ731016 Sequence	
12	451	32.7	188646	9	AC027045		AC027045 Homo sapi	

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_hlc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID		Description
c	1	621	45.0	631	1	AI091419	AI091419 ow62e03.x
c	2	551	40.0	632	1	AI741629	AI741629 wg28f07.x
c	3	495	35.9	562	1	AI458236	AI458236 tj53e07.x
c	4	485	35.2	632	1	AI741640	AI741640 wg28g07.x
	5	478	34.7	483	9	AY421548	AY421548 Homo sapi
c	6	473	34.3	473	1	AI376903	AI376903 tc27f05.x
c	7	469	34.0	469	1	AI141463	AI141463 qa67d12.x
c	8	414	30.0	558	1	AI222126	AI222126 qh02g04.x
c	9	261	18.9	505	1	AA953672	AA953672 oo02e08.s
	10	257	18.6	309	7	F26544	F26544 HSPD14061 H
c	11	256	18.6	307	1	AI470361	AI470361 tj42f03.x
c	12	254	18.4	477	1	AI168267	AI168267 oo10c10.x
	13	248	18.0	267	9	AY421549	AY421549 Pan trogl
	14	247	17.9	274	7	F35823	F35823 HSPD32901 H
c	15	243	17.6	396	1	AA928254	AA928254 on79a08.s
c	16	222	16.1	480	1	AI022337	AI022337 ow95a11.x